

SEQUENCE LISTING

<110> Ozelius, Laurie J.
Breakefield, Xandra O.

<120> TORSIN, TORSIN-RELATED GENES, AND
METHODS OF DETECTING NEURONAL DISEASES

<130> 0838.1001009

<150> 09/461,921

<151> 1999-12-15

<150> US 09/218,363

<151> 1998-12-22

<150> US 09/099,454

<151> 1998-06-18

<150> US 60/050,244

<151> 1997-06-19

<160> 90

<170> FastSEQ for Windows Version 4.0

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<212> DNA

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aacaagcagg gtggcgcggg tccgggc atg aag ctg gcc cgg gcc gtg ctg gcc 594
Met Lys Leu Gly Arg Ala Val Leu Gly
1 5
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ctg ctg ctg ctg gcg ccg tcc gtg gtg cag gcg gtg gag ccc atc agc 642
Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala Val Glu Pro Ile Ser
10 15 20 25
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Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly Tyr Ile Tyr Pro Arg	
30 35 40	
ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag aag cgg agc ctt agc	738
Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln Lys Arg Ser Leu Ser	
45 50 55	
cgg gag gca ctg cag aag gat ctg gac gac aac ctc ttt gga cag cat	786
Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn Leu Phe Gly Gln His	
60 65 70	
ctt gca aag aaa atc atc tta aat gcc gtg ttt ggt ttc ata aac aac	834
Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe Gly Phe Ile Asn Asn	
75 80 85	
cca aag ccc aag aaa cct ctc acg ctc tcc ctg cac ggg tgg aca ggc	882
Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly	
90 95 100 105	
acc ggc aaa aat ttc gtc agc aag atc atc gca gag aat att tac gag	930
Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu	
110 115 120	
ggt ggt ctg aac agt gac tat gtc cac ctg ttt gtg gcc aca ttg cac	978
Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His	
125 130 135	
ttt cca cat gct tca aac atc acc ttg tac aag gat cag tta cag ttg	1026
Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu	
140 145 150	
tgg att cga ggc aac gtg agt gcc tgt gcg agg tcc atc ttc ata ttt	1074
Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe	
155 160 165	
gat gaa atg gat aag atg cat gca ggc ctc ata gat gcc atc aag cct	1122
Asp Glu Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro	
170 175 180 185	
ttc ctc gac tat tat gac ctg gtg gat ggg gtc tcc tac cag aaa gcc	1170
Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala	
190 195 200	
atg ttc ata ttt ctc agc aat gct gga gca gaa agg atc aca gat gtg	1218
Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val	
205 210 215	
gct ttg gat ttc tgg agg agt gga aag cag agg gaa gac atc aag ctc	1266
Ala Leu Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu	
220 225 230	
aaa gac att gaa cac gcg ttg tct gtg tcg gtt ttc aat aac aag aac	1314
Lys Asp Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn	
235 240 245	

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agt ggc ttc tgg cac agc agc tta att gac cgg aac ctc att gat tat 1362
Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr
250                255                260                265

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ttt gtt ccc ttc ctc ccc ctg gaa tac aaa cac cta aaa atg tgt atc 1410
Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile
                270                275                280

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cga gtg gaa atg cag tcc cga ggc tat gaa att gat gaa gac att gta 1458
Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile Asp Glu Asp Ile Val
                285                290                295

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agc aga gtg gct gag gag atg aca ttt ttc ccc aaa gag gag aga gtt 1506
Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro Lys Glu Glu Arg Val
                300                305                310

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ttc tca gat aaa ggc tgc aaa acg gtg ttc acc aag tta gat tat tac 1554
Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr Lys Leu Asp Tyr Tyr
                315                320                325

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tac gat gat tgacagtcac gattggcagc cggagtcact gcctggagtt 1603
Tyr Asp Asp
330

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ggaaaagaaa caacactcag tccttcacaca cttccacccc cagctccttt ccctggaaga 1663
ggaatccagt gaatgttcct gtttgatgtg acaggaattc tccctggcat tgtttccacc 1723
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<210> 2

<211> 332

<212> PRT

<213> Homo sapien

<400> 2

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Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
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          20          25          30
Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
          35          40          45
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
          50          55          60
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
65          70          75          80
Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
          85          90          95

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Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160
 Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
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 Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

<210> 3
 <211> 3568
 <212> DNA
 <213> Homo sapien

 <220>
 <221> CDS
 <222> (994)...(1863)

 <221> misc_feature
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 taactgcaac ctccgcctcc tgggttcaag agattctcct gcctcaacct ccgagtagct 180
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 gttcaagaga ttctnctgcc tcaactcccg agtagctggg attataggng nccgcnacca 360
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 ctgggattac aggcgtgaca ccgngcccgg sccgaaaaaa twttttttaa agaaaaaggg 660
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 gncctmacc aaccatggcc gncccnaagg gagtggggcg ggtctgcggg gcggaagtga 780
 cgsacgagag gaagtccgct ctgcgcttgg ccgcggggcg cctggctcag tggcttctgc 840

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 gcaggtcggc catcaccggc tacctgtcct aca atg aca tct act gcc cgt tcg 1014
 Met Thr Ser Thr Ala Arg Ser
 1 5

ccg agt gct gcc ggc gag gag cgg ccg ctc aac gct tcg gct ctc aag 1062
 Pro Ser Ala Ala Gly Glu Glu Arg Pro Leu Asn Ala Ser Ala Leu Lys
 10 15 20

ctg gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg 1110
 Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
 25 30 35

att ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa 1158
 Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
 40 45 50 55

cca ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt 1206
 Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
 60 65 70

gtc agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt 1254
 Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
 75 80 85

aac ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag 1302
 Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
 90 95 100

aag ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat 1350
 Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
 105 110 115

gtg agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa 1398
 Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
 120 125 130 135

ttg cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac 1446
 Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
 140 145 150

gag cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc 1494
 Glu Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu
 155 160 165

agc aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg 1542
 Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
 170 175 180

cgg gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct 1590
 Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
 185 190 195

gta ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac 1638
 Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
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Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
                220                225                230

cct ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg 1734
Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
                235                240                245

gcc cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag 1782
Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
                250                255                260

gaa atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc 1830
Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly
                265                270                275

tgc aag act gtg cag tcg cgg ctg gat ttc cac tgagctccta tccagatggg 1883
Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
280                285                290

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gagaagaggt ctcaactcgt catccaagct ggagtgcagt ggtgcaatcc tcaactcact 2063
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<212> PRT
<213> Homo sapien

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Gln His Leu Ala Thr Glu Val Ile Phe Lys Ala Leu Thr Gly Phe Arg
 35 40 45
 Asn Asn Lys Asn Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp
 50 55 60
 Ala Gly Thr Gly Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu
 65 70 75 80
 His Pro Lys Gly Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr
 85 90 95
 Leu His Phe Pro His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu
 100 105 110
 Gln Lys Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe
 115 120 125
 Ile Phe Asp Glu Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile
 130 135 140
 Lys Pro Phe Leu Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Arg
 145 150 155 160
 Lys Ala Ile Phe Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr
 165 170 175
 Lys Thr Ala Leu Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile
 180 185 190
 Gln Leu Lys Asp Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn
 195 200 205
 Lys His Ser Gly Leu Trp His Ser Gly Leu Ile Asp Lys Asn Leu Ile
 210 215 220
 Asp Tyr Phe Ile Pro Phe Leu Pro Leu Glu Tyr Arg His Val Lys Met
 225 230 235 240
 Cys Val Arg Ala Glu Met Arg Ala Arg Gly Ser Ala Ile Asp Glu Asp
 245 250 255
 Ile Val Thr Arg Val Ala Glu Glu Met Thr Phe Phe Pro Arg Asp Glu
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 Phe His
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<222> (43)...(1038)

<400> 5

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 Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser Val Val Gln Ala
 5 10 15 20

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 Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly Val Leu Thr Gly
 25 30 35

tac atc tac ccg cgt ctc tac tgc ctc ttc gcc gag tgc tgc ggg cag	198
Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu Cys Cys Gly Gln	
40 45 50	
aag cgg agc ctt agc cgg gag gca ctg cag aag gat ctg gac gac aac	246
Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp Leu Asp Asp Asn	
55 60 65	
ctc ttt gga cag cat ctt gca aag aaa atc atc tta aat gcc gtg ttt	294
Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu Asn Ala Val Phe	
70 75 80	
ggg ttc ata aac aac cca aag ccc aag aaa cct ctc acg ctc tcc ctg	342
Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu Thr Leu Ser Leu	
85 90 95 100	
cac ggg tgg aca ggc acc ggc aaa aat ttc gtc agc aag atc atc gca	390
His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser Lys Ile Ile Ala	
105 110 115	
gag aat att tac gag ggt ggt ctg aac agt gac tat gtc cac ctg ttt	438
Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr Val His Leu Phe	
120 125 130	
gtg gcc aca ttg cac ttt cca cat gct tca aac atc acc ttg tac aag	486
Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile Thr Leu Tyr Lys	
135 140 145	
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Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser Ala Cys Ala Arg	
150 155 160	
tcc atc ttc ata ttt gat gaa atg gat aag atg cat gca ggc ctc ata	582
Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His Ala Gly Leu Ile	
165 170 175 180	
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Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu Val Asp Gly Val	
185 190 195	
tcc tac cag aaa gcc atg ttc ata ttt ctc agc aat gct gga gca gaa	678
Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn Ala Gly Ala Glu	
200 205 210	
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215 220 225	
gaa gac atc aag ctc aaa gac att gaa cac gcg ttg tct gtg tcg gtt	774
Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu Ser Val Ser Val	
230 235 240	
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Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser Leu Ile Asp Arg	
245 250 255 260	
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Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu Glu Tyr Lys His	
265 270 275	

cta aaa atg tgt atc cga gtg gaa atg cag tcc cga ggc tat gaa att 918
 Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg Gly Tyr Glu Ile
 280 285 290

gat gaa gac att gta agc aga gtg gct gag gag atg aca ttt ttc ccc 966
 Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met Thr Phe Phe Pro
 295 300 305

aaa gag gag aga gtt ttc tca gat aaa ggc tgc aaa acg gtg ttc acc 1014
 Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys Thr Val Phe Thr
 310 315 320

aag tta gat tat tac tac gat gat tgacagtcac gattggcagc cggagtcact 1068
 Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

gcctggagtt ggaaaagaaa caacactcag tccttccaca cttccacccc cagctccttt 1128
 ccctggaaga ggaatccagt gaatgttcct gtttgatgtg acaggaattc tccctggcat 1188
 tgtttccacc ccctgggtgcc tgcaggccac ccagggacca cgggcgagga cgtgaagcct 1248
 cccgaacacg cacagaagga aggagccagc tcccagccca ctcacgcag ggctcatgat 1308
 tttttacaaa ttatgtttta attccaagtg tttctgtttc aaggaaggat gaataagttt 1368
 tattgaaaat gtggttaactt tatttaaaat gatttttaac attatgagag actgctcaga 1428
 ttctaagttg ttggccttgt gtgtgtgttt ttttttaagt tctcatcatt attacataga 1488
 ctgtgaagta tctttactgg aaatgagccc aagcacacat gcatggcatt tgttcctgaa 1548
 caggagggca tccttgggga tgtggctgga gcatgagcca gctctgtccc aggatgggcc 1608
 cagcggatgc tgccaggggc agtgaagtgt ttaggtgaag gacaagtagg taagaggacg 1668
 ccttcaggca ccacagataa gcctgaaaca gcctctccaa gggttttcac cttagcaaca 1728
 atgggagctg tgggagtgat tttggccaca ctgtcaacat ttgttagaac cagtcttttg 1788
 aaagaaaagt atttccaact tgtcacttgc cagtcactcc gttttgcaaa aggtggccct 1848
 tcactgtcca ttccaaatag cccacacgtg ctctctgctg gattctaaat tatgtgaatt 1908
 ttgccatatt aaatcttctt catttatact attatttggt acgttcaatc agaatccccg 1968
 aaacctccta taaagcttag ctgccccctt tgaggatgct gagaacgggtg tctttcttta 2028
 taaatgcaaa tggctaccgt tttaacaataa aattttgcat gtgc 2072

<210> 6
 <211> 332
 <212> PRT
 <213> Homo sapien

<400> 6
 Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
 1 5 10 15
 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
 165 170 175
 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
 180 185 190
 Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
 195 200 205
 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
 210 215 220
 Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
 225 230 235 240
 Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
 245 250 255
 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
 260 265 270
 Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
 275 280 285
 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
 290 295 300
 Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
 305 310 315 320
 Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
 325 330

<210> 7

<211> 2504

<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (2)...(799)

<400> 7

g gat ttg gag gag aag ctg ttt gga cag cat cta gcc acg gaa gtg att 49
 Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile
 1 5 10 15

ttc aag gcg ctg act ggc ttc agg aac aac aaa aat ccc aag aaa cca 97
 Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
 20 25 30

ctg acc ctt tcc tta cac ggc tgg gct ggc aca ggc aag aat ttt gtc 145
 Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val
 35 40 45

agt caa att gtg gct gaa aat ctt cac cca aaa ggt ctg aag agt aac 193
 Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
 50 55 60

ttt gtc cac ctg ttt gta tcg act ctg cac ttc cct cat gag cag aag 241
 Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys
 65 70 75 80

ata aaa ctg tac cag gac cag tta cag aag tgg atc cgc ggt aat gtg 289
 Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val
 85 90 95

agt gca tgt gcg aac tct gtt ttc ata ttt gac gag atg gat aaa ttg 337
 Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu
 100 105 110

cac ccc ggg atc att gac gca atc aag ccg ttt cta gac tac tac gag 385
 His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu
 115 120 125

cag gtt gac gga gtg tct tac cgc aaa gcc atc ttc atc ttt ctc agc 433
 Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser
 130 135 140

aat gca ggc ggg gac ctt ata act aag acg gct ctt gac ttt tgg cgg 481
 Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg
 145 150 155 160

gcc gga aga aag agg gaa gac att cag ctg aag gac ctg gaa cct gta 529
 Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val
 165 170 175

ctg tct gtc gga gtc ttc aat aat aaa cac agt ggc ctg tgg cac agt 577
 Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser
 180 185 190

gga ctg atc gac aaa aac ctc att gat tac ttt atc ccc ttc ctg cct 625
 Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro
 195 200 205

ttg gag tac aga cat gtg aaa atg tgt gtg agg gcc gag atg agg gcc 673
 Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala
 210 215 220

cgt ggt tct gcc ata gat gaa gac att gtc aca aga gtg gca gag gaa 721
 Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu
 225 230 235 240

atg acg ttt ttc ccc aga gac gag aaa atc tac tca gac aag ggc tgc 769
 Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys
 245 250 255

aag act gtg cag tcg cgg ctg gat ttc cac tgagctccta tccagatggg 819
 Lys Thr Val Gln Ser Arg Leu Asp Phe His
 260 265

gtaggagaca gctgggaggc tccgcacgcc agaggccttg cctttcagaa gaaccctgaa 879
 gaccgctttg gggttttgcc tgtttgcacc ttagactttt gggatatagaa tctttttttt 939
 gagaagaggt ctcactccgt catccaagct ggagtgcagt ggtgcaatcc tcaactcact 999
 gcaacctccg ctcccggttt gactgattct catgcctcag cctcccagat agctgggatt 1059
 acaggcatga gccactgtgc ccagctggga tatagaatct aagagttgat tgtggaaaac 1119
 acgtgaatct attgcgcgca tttgtcattt agcaagatgg cagcagtcca gctgttcttt 1179
 gcagctggag atgaactttt aaaaatcccc ttcacactta atgtactgac cgagacagaa 1239
 gtacctgaaa acagctgtgc atggcaggcc cggcaatagc ttctgaccca cagcaccgcg 1299
 gcctcagaag ctacggtcac aactaaagga gtccagggac ttgctgcagg ctgggggggca 1359
 ctgggtggtt ctcaccagca ggctgcgggg cactgtgttc tcattggcca aaaacatcct 1419
 tttgctctgt ctggttcttt acacagagtt cactgacttg aagtatactc agttaaaatc 1479
 ggggctggag gtgcagacgg tgtctgaccg gaggatgtgg ccgtgcccgc cgagcactct 1539
 tgatctggag tgacctgtgt gtgtgtgtgg ggggggggtg ggcccttcacc taagacctct 1599
 gcagcagacc tggacagaca gggccctccc gcctgtccat cgctctagct gctaatacag 1659
 ccctggctgt ggaatccttc accgtctcag ctggatatcag cccagcctg ccttggtgcc 1719
 atatctcagc ttggatctct gctagagtcc cccaacccat atatcataga gttgaatcac 1779

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aatgagaccg ttggccttga atttgagtcg ttgggtccca tgggtgagatg cttgttaaga 1839
ctttatactt ggggtcaatct ctcactttat tttgtagaac catttgaaat cctaggatgt 1899
gcttgttctg gaaggatgac atggggccag actgaacaag tcagcttgat gatcttaaat 1959
gatggaagta taggacgttg cttattttta aacaagggaa ggacacaaaa tggaatgact 2019
gccttagtcc tttctcagat actccttaaa acaatttttt attgttttaa tttgtggtaa 2079
tacatgggtca caaccgtgga tcaaacaagg tcagtctaaa gtggcaggtc ctaggtgtga 2139
cctgatacca ccaccctttg tggcagcacc gggctggact gccctgatcc ctgggacgtg 2199
agacttagct tccagccagt gtgaatcatt gtatctgtct cataatcaca gcacagctgc 2259
agacacaaca acgtgcagca ttttttacat aaaaatatgg tagaattaat ttatgacatg 2319
gaaatgcctt acgtgggtatc acacttagtc ttgaaaaaaa caccaagggtg acgttttaaaa 2379
tttttagtac atatcctcaa attggagcta agttatactt cttttataac cttttgggca 2439
tctggtcgag agaagacaag attttctcta tttacagtga ggcaataaat atgtttgccca 2499
cctttt                                     2504

```

<210> 8

<211> 266

<212> PRT

<213> Homo sapien

<400> 8

```

Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val Ile
1      5      10      15
Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys Pro
20      25      30
Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe Val
35      40      45
Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser Asn
50      55      60
Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln Lys
65      70      75      80
Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn Val
85      90      95
Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys Leu
100     105     110
His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Glu
115     120     125
Gln Val Asp Gly Val Ser Tyr Arg Lys Ala Ile Phe Ile Phe Leu Ser
130     135     140
Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp Arg
145     150     155     160
Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro Val
165     170     175
Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His Ser
180     185     190
Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu Pro
195     200     205
Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg Ala
210     215     220
Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu Glu
225     230     235     240
Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gly Cys
245     250     255
Lys Thr Val Gln Ser Arg Leu Asp Phe His
260     265

```

<210> 9

<211> 332

<212> PRT

<213> Homo sapien

<400> 9

```

Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Leu Ala Pro Ser
 1          5          10          15
Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
      20          25          30
Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
      35          40          45
Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
      50          55          60
Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
65          70          75          80
Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
      85          90          95
Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
      100          105          110
Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
      115          120          125
Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
130          135          140
Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
145          150          155          160
Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
      165          170          175
Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
      180          185          190
Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
195          200          205
Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
210          215          220
Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
225          230          235          240
Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
      245          250          255
Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
260          265          270
Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
275          280          285
Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
290          295          300
Thr Phe Phe Pro Lys Glu Glu Pro Val Phe Ser Asp Lys Gly Cys Lys
305          310          315          320
Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
      325          330

```

<210> 10

<211> 267

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(267)

<223> Xaa = any amino acid

<400> 10

```

Leu Asp Leu Glu Glu Lys Leu Phe Gly Gln His Leu Ala Thr Glu Val
 1          5          10          15
Ile Phe Lys Ala Leu Thr Gly Phe Arg Asn Asn Lys Asn Pro Lys Lys
      20          25          30

```

```

Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly Lys Asn Phe
    35          40          45
Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly Leu Lys Ser
    50          55          60
Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro His Glu Gln
    65          70          75          80
Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile Arg Gly Asn
    85          90          95
Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu Met Asp Lys
    100          105          110
Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr
    115          120          125
Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe Ile Phe Leu
    130          135          140
Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu Asp Phe Trp
    145          150          155          160
Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp Leu Glu Pro
    165          170          175
Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly Leu Trp His
    180          185          190
Ser Gly Leu Ile Asp Lys Asn Leu Ile Asp Tyr Phe Ile Pro Phe Leu
    195          200          205
Pro Leu Glu Tyr Arg His Val Lys Met Cys Val Arg Ala Glu Met Arg
    210          215          220
Ala Arg Gly Ser Ala Ile Asp Glu Asp Ile Val Thr Arg Val Ala Glu
    225          230          235          240
Glu Met Thr Phe Phe Pro Arg Asp Glu Lys Ile Tyr Ser Asp Lys Gln
    245          250          255
Cys Lys Thr Val Gln Ser Arg Leu Asp Phe His
    260          265

```

```

<210> 11
<211> 334
<212> PRT
<213> C. elegans

```

```

<400> 11
Met Trp Met Lys Leu Asp Tyr Val Leu Leu Leu Leu Phe His Leu Cys
    1          5          10          15
Phe Val Asn Thr Glu Leu Ile Ser Val Ile Thr Gly Lys Ile Lys Asp
    20          25          30
Ser Gly Thr Thr Ile Ala Ile Ser Ala Gly Ala Phe Trp Gly Leu Lys
    35          40          45
Asp Arg Leu Lys Cys Tyr Leu Tyr Glu Cys Cys His Glu Pro Asp Val
    50          55          60
Asn Phe Asn Tyr His Thr Leu Asp Ala Asp Ile Ala Asn Leu Leu Phe
    65          70          75          80
Gly Gln His Leu Val Lys Asp Val Val Val Asn Ser Ile Lys Ser His
    85          90          95
Trp Tyr Asn Glu Asn Pro Arg Lys Pro Leu Val Leu Ser Phe His Gly
    100          105          110
Tyr Thr Gly Ser Gly Lys Asn Tyr Val Ala Glu Ile Ile Ala Asn Asn
    115          120          125

Thr Phe Arg Leu Gly Leu Arg Ser Thr Phe Val Gln His Ile Val Ala
    130          135          140
Thr Asn Asp Phe Pro Asp Lys Asn Lys Leu Glu Glu Tyr Gln Val Glu
    145          150          155          160

```

```

Leu Arg Asn Arg Ile Leu Thr Thr Val Gln Lys Cys Gln Arg Ser Ile
      165      170      175
Phe Ile Phe Asp Glu Ala Asp Lys Leu Pro Glu Gln Leu Leu Gly Ala
      180      185      190
Ile Lys Pro Phe Leu Asp Tyr Tyr Ser Thr Ile Ser Gly Val Asp Phe
      195      200      205
Arg Arg Ser Ile Phe Ile Leu Leu Ser Asn Lys Gly Gly Gly Glu Ile
      210      215      220
Ala Arg Ile Thr Lys Glu Gln Tyr Glu Ser Gly Tyr Pro Arg Glu Gln
      225      230      235      240
Leu Arg Leu Glu Ala Phe Glu Arg Glu Leu Met Asn Phe Ser Tyr Asn
      245      250      255
Glu Lys Gly Gly Leu Gln Met Ser Glu Leu Ile Ser Asn His Leu Ile
      260      265      270
Asp His Phe Val Pro Phe Leu Pro Leu Gln Arg Glu His Val Arg Ser
      275      280      285
Cys Val Gly Ala Tyr Leu Arg Lys Arg Gly Arg Gly Asp Leu Val Ser
      290      295      300
Asn Val Asp Phe Val Glu Arg Val Leu Asn Ser Leu Gln Tyr Phe Pro
      305      310      315      320
Glu Ser Ser Lys Ala Phe Ser Ser Ser Gly Cys Lys Arg Val
      325      330

```

```

<210> 12
<211> 268
<212> PRT
<213> Homo sapien

```

```

<400> 12
Leu Glu Cys Asp Leu Ala Gln His Leu Ala Gly Gln His Leu Ala Lys
  1      5      10      15
Ala Leu Val Val Lys Ser Leu Lys Ala Phe Val Gln Asp Pro Ala Pro
      20      25      30
Ser Lys Pro Leu Val Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys
      35      40      45
Ser Tyr Val Ser Ser Leu Leu Ala Gln His Leu Phe Arg Asp Gly Leu
      50      55      60
Arg Ser Pro His Val His His Phe Ser Pro Ile Ile His Phe Pro His
      65      70      75      80
Pro Ser Arg Thr Glu Gln Tyr Lys Lys Glu Leu Lys Ser Trp Val Gln
      85      90      95
Gly Asn Thr Ala Cys Glu Arg Ser Leu Phe Leu Phe Asp Glu Met Asp
      100      105      110
Lys Leu Pro Pro Gly Leu Met Glu Val Leu Gln Pro Phe Leu Gly Pro
      115      120      125
Ser Trp Val Val Tyr Gly Thr Asn Tyr Arg Lys Ala Ile Phe Ile Phe
      130      135      140
Ile Ser Asn Ala Gly Gly Glu Cys Ile Asn Gln Val Ala Leu Glu Ala
      145      150      155      160
Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu Val Glu
      165      170      175
Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly Phe Trp
      180      185      190
Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val Pro Phe
      195      200      205
Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn Glu Leu
      210      215      220
Ala Gln Leu Gly Leu Glu Pro Ala Arg Arg Trp Phe Arg Arg Cys Trp
      225      230      235      240

```

```
<210> 13
<211> 177
<212> PRT
<213> Murine

<220>
<221> VARIANT
<222> (1)...(177)
<223> Xaa = Any Amino Acid
```

```
<210> 14
<211> 214
<212> PRT
<213> Murine
```

<400> 14															
Glu	Glu	His	Pro	Leu	Val	Phe	Leu	Phe	Leu	Gly	Ser	Ser	Gly	Ile	Gly
1				5					10					15	
Lys	Thr	Glu	Leu	Ala	Lys	Gln	Thr	Ala	Lys	Tyr	Met	His	Lys	Asp	Ala
			20					25					30		
Lys	Lys	Gly	Phe	Ile	Arg	Leu	Asp	Met	Ser	Glu	Phe	Gln	Glu	Arg	His
		35				40						45			
Glu	Val	Ala	Lys	Phe	Ile	Gly	Ser	Pro	Arg	Gly	Tyr	Ile	Gly	His	Glu
	50				55						60				
Glu	Gly	Gly	Gln	Leu	Thr	Lys	Lys	Leu	Lys	Gln	Cys	Pro	Asn	Ala	Val
65				70						75					80


```

Val Leu Phe Asp Glu Val Asp Lys Ala His Pro Asp Val Leu Thr Ile
      85      90      95
Met Leu Gln Leu Phe Asp Glu Gly Arg Leu Thr Asp Gly Lys Gly Lys
      100      105      110
Thr Ile Asp Cys Lys Asp Ala Ile Phe Ile Met Thr Ser Asn Val Ala
      115      120      125
Ser Asp Glu Ile Ala Gln His Ala Leu Gln Leu Arg Gln Glu Ala Leu
      130      135      140
Glu Met Ser Arg Asn Arg Ile Ala Glu Asn Leu Gly Asp Val Gln Met
      145      150      155      160
Ser Asp Lys Ile Thr Ile Ser Lys Asn Phe Lys Glu Asn Val Ile Arg
      165      170      175
Pro Ile Leu Lys Ala His Phe Arg Arg Asp Glu Phe Leu Gly Arg Ile
      180      185      190
Asn Glu Ile Val Tyr Phe Leu Pro Phe Cys His Ser Glu Leu Ile Gln
      195      200      205
Leu Val Asn Lys Glu Leu
      210

```

```

<210> 15
<211> 185
<212> PRT
<213> Unknown

```

```

<220>
<223> Soybean

```

```

<400> 15
Pro Gln Gln Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val
  1      5      10      15
Gly Lys Thr Glu Leu Ala Lys Ala Leu Ala Glu Gln Leu Phe Asp Asn
      20      25      30
Glu Asn Gln Leu Val Arg Ile Asp Met Ser Glu Tyr Met Glu Gln His
      35      40      45
Ser Val Ser Arg Leu Ile Gly Ala Pro Pro Gly Tyr Val Gly His Glu
      50      55      60
Glu Gly Gly Gln Leu Thr Glu Ala Val Arg Arg Arg Pro Tyr Ser Val
      65      70      75      80
Val Leu Phe Asp Glu Val Glu Lys Ala His Thr Ser Val Phe Asn Ile
      85      90      95
Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
      100      105      110
Thr Val Asp Phe Arg Asn Thr Val Ile Ile Met Thr Ser Asn Leu Gly
      115      120      125
Ala Glu His Leu Leu Ser Gly Ser Gln Lys Cys Thr Met Gln Val Ala
      130      135      140
Arg Asp Arg Val Met Glu Gln Glu Arg Arg Gln Phe Arg Pro Glu Leu
      145      150      155      160
Leu Asn Arg Leu Asp Glu Ile Val Val Phe Asp Pro Leu Ser His Asp
      165      170      175
Gln Leu Arg Lys Val Ala Arg Leu Met
      180      185

```

```

<210> 16
<211> 194
<212> PRT
<213> Homo sapien

```

```

<400> 16

```

```

Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly
 1          5          10          15
Lys Asn Phe Val Ser Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly
 20          25          30
Leu Asn Ser Asp Tyr Val His Leu Phe Val Ala Thr Leu His Phe Pro
 35          40          45
His Ala Ser Asn Ile Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile
 50          55          60
Arg Gly Asn Val Ser Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu
 65          70          75          80
Met Asp Lys Met His Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu
 85          90          95
Asp Tyr Tyr Asp Leu Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe
100          105          110
Ile Phe Leu Ser Asn Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu
115          120          125
Asp Phe Trp Arg Ser Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp
130          135          140
Ile Glu His Ala Leu Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly
145          150          155          160
Phe Trp His Ser Ser Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val
165          170          175
Pro Phe Leu Pro Leu Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val
180          185          190
Glu Met

```

```

<210> 17
<211> 194
<212> PRT
<213> Homo sapien

```

```

<220>
<221> VARIANT
<222> (1)...(194)
<223> Xaa = Any Amino Acid

```

```

<400> 17
Pro Lys Lys Pro Leu Thr Leu Ser Leu His Gly Trp Ala Gly Thr Gly
 1          5          10          15
Lys Asn Phe Val Ser Gln Ile Val Ala Glu Asn Leu His Pro Lys Gly
 20          25          30
Leu Lys Ser Asn Phe Val His Leu Phe Val Ser Thr Leu His Phe Pro
 35          40          45
His Glu Gln Lys Ile Lys Leu Tyr Gln Asp Gln Leu Gln Lys Trp Ile
 50          55          60
Arg Gly Asn Val Ser Ala Cys Ala Asn Ser Val Phe Ile Phe Asp Glu
 65          70          75          80
Met Asp Lys Leu His Pro Gly Ile Ile Asp Ala Ile Lys Pro Phe Leu
 85          90          95
Asp Tyr Tyr Glu Gln Val Asp Gly Val Ser Tyr Xaa Lys Ala Ile Phe
100          105          110
Ile Phe Leu Ser Asn Ala Gly Gly Asp Leu Ile Thr Lys Thr Ala Leu
115          120          125
Asp Phe Trp Arg Ala Gly Arg Lys Arg Glu Asp Ile Gln Leu Lys Asp
130          135          140
Leu Glu Pro Val Leu Ser Val Gly Val Phe Asn Asn Lys His Ser Gly
145          150          155          160

```

```
<210> 18
<211> 192
<212> PRT
<213> C. elegans
```

Pro 1	Arg	Lys	Pro	Leu 5	Val	Leu	Ser	Phe	His 10	Gly	Tyr	Thr	Gly	Ser 15	Gly
Lys	Asn	Tyr	Val 20	Ala	Glu	Ile	Ile	Ala 25	Asn	Asn	Thr	Phe	Arg 30	Leu	Gly
Leu	Arg	Ser 35	Thr	Phe	Val	Gln	His 40	Ile	Val	Ala	Thr	Asn 45	Asp	Phe	Pro
Asp	Lys 50	Asn	Lys	Leu	Glu	Glu 55	Tyr	Gln	Val	Glu	Leu 60	Arg	Asn	Arg	Ile
Leu 65	Thr	Thr	Val	Gln 70	Lys	Cys	Arg	Ser	Ile	Phe 75	Ile	Phe	Asp	Glu	Ala 80
Asp	Lys	Leu	Pro 85	Glu	Gln	Leu	Leu	Gly	Ala 90	Ile	Lys	Pro	Phe 95	Leu	Asp
Tyr	Tyr	Ser 100	Thr	Ile	Ser	Gly	Val	Asp 105	Phe	Arg	Arg	Ser	Ile 110	Phe	Ile
Leu	Leu	Ser 115	Asn	Lys	Gly	Gly	Gly 120	Glu	Ile	Ala	Arg	Ile 125	Thr	Lys	Glu
Gln	Tyr 130	Glu	Ser	Gly	Tyr	Pro 135	Arg	Glu	Gln	Leu	Arg 140	Leu	Glu	Ala	Phe
Glu 145	Arg	Glu	Leu	Met 150	Asn	Phe	Ser	Tyr	Asn	Glu 155	Lys	Gly	Gly	Leu	Gln 160
Met	Ser	Glu	Leu 165	Ile	Ser	Asn	His	Leu 170	Ile	Asp	His	Phe	Val 175	Pro	Phe
Leu	Pro	Leu	Gln 180	Arg	Glu	His	Val	Arg 185	Ser	Cys	Val	Gly	Ala 190	Tyr	Leu

```
<210> 19
<211> 194
<212> PRT
<213> Homo sapien
```

Pro 1	Ser	Lys	Pro	Leu 5	Val	Leu	Ser	Leu	His 10	Gly	Trp	Thr	Gly	Thr 15	Gly
Lys	Ser	Tyr	Val	Ser	Ser	Leu	Leu	Ala	Gln	His	Leu	Phe	Arg	Asp	Gly
		20						25					30		
Leu	Arg	Ser	Pro	His	Val	His	His	Phe	Ser	Pro	Ile	Ile	His	Phe	Pro
		35					40					45			
His	Pro	Ser	Arg	Thr	Glu	Gln	Tyr	Lys	Lys	Glu	Leu	Lys	Ser	Trp	Val
	50					55					60				
Gln	Gly	Asn	Leu	Thr	Ala	Cys	Glu	Arg	Ser	Leu	Phe	Leu	Phe	Asp	Glu
65					70					75					80
Met	Asp	Lys	Leu	Pro	Pro	Gly	Leu	Met	Glu	Val	Leu	Gln	Pro	Phe	Leu
			85					90						95	
Gly	Pro	Ser	Trp	Val	Val	Tyr	Gly	Thr	Asn	Tyr	Arg	Lys	Ala	Ile	Phe
			100					105					110		
Ile	Phe	Ile	Ser	Asn	Ala	Gly	Gly	Glu	Gln	Ile	Asn	Gln	Val	Ala	Leu
		115					120					125			

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Glu Ala Trp Arg Thr Asn Arg Asp Arg Glu Glu Ile Ser Leu Gln Glu
130 135 140
Val Glu Pro Val Ile Ser Arg Ala Val Met Asp Asn Pro Gln His Gly
145 150 155 160
Phe Trp Arg Ser Gly Ile Met Glu Glu His Leu Leu Asp Ala Val Val
165 170 175
Pro Phe Leu Pro Leu Gln Arg His His Val Arg His Cys Val Leu Asn
180 185 190
Glu Leu

<210> 20
<211> 128
<212> PRT
<213> Murine

<220>
<221> VARIANT
<222> (1)...(128)
<223> Xaa = Any Amino Acid

<400> 20
Ala Ala Ala Leu His Gln Thr Leu Phe Ile Phe Asp Glu Ala Glu Lys
1 5 10 15
Leu His Pro Gly Leu Leu Glu Val Leu Gly Pro His Leu Glu Arg Arg
20 25 30
Ala Pro Glu Xaa Xaa Gly Leu Ser Leu Xaa Trp Thr Ile Phe Leu Phe
35 40 45
Leu Ser Asn Leu Arg Gly Asp Ile Ile Asn Glu Val Val Leu Lys Leu
50 55 60
Leu Lys Ala Gly Trp Ser Arg Glu Glu Ile Thr Met Glu His Leu Glu
65 70 75 80
Pro His Leu Gln Ala Glu Ile Val Asp Asp His Arg Gln Trp Leu Trp
85 90 95
His Ser Arg Leu Val Lys Glu Asn Leu Ile Asp Tyr Phe Ile Pro Phe
100 105 110
Leu Pro Leu Glu Tyr Arg His Val Arg Leu Cys Ala Arg Asp Ala Phe
115 120 125

<210> 21
<211> 253
<212> DNA
<213> Homo sapien

<400> 21
cctggaatac aaacacctaa aaatgtgtat ccgagtggaa atgcagtccc gaggctatga 60
aattgatgaa gacattgtaa gcagagtggc tgaggagatg acatttttcc ccaaagagga 120
gagagttttc tcagataaag gctgcaaaac ggtgttcacc aagtttagatt attactacga 180
tgattgacag tcatgattgg cagccggagt cactgcctgg agttggaaag aaacaacact 240
cagtccttcc acc 253

<210> 22
<211> 253
<212> DNA
<213> Homo sapien

<400> 22
ggaccttatg tttgtggatt ttacacata ggctcacctt tacgtcaggg tccgatactt 60

```

taactacttc tgtaacattc gtctcacgga ctcctctact gtaaaaagg gtttctcctc 120
tctcaaaaga gtctatttcc gacgttttgc caccaagtgg ttcaatctaa taatgatgct 180
actaactgtc agtactaacc gtcggcctca gtgacggacc tcaacctttc tttgttgatga 240
gtcaggaagg tgg                                     253

```

```

<210> 23
<211> 7
<212> PRT
<213> Homo sapien

```

```

<400> 23
Phe Phe Thr Met Glu Ala Val
 1                5

```

```

<210> 24
<211> 21
<212> DNA
<213> Homo sapien

```

```

<400> 24
gtggctgaga tgacattttt c                                     21

```

```

<210> 25
<211> 24
<212> DNA
<213> Homo sapien

```

```

<400> 25
gtggctgagg agatgacatt tttc                                     24

```

```

<210> 26
<211> 8
<212> PRT
<213> Homo sapien

```

```

<400> 26
Phe Phe Thr Met Glu Glu Ala Val
 1                5

```

```

<210> 27
<211> 205
<212> DNA
<213> Synthetic

```

```

<400> 27
cctggaatac aaacacctaa aaatgtgtat ccgagtggaa atgcagtccc gaggctatga 60
aattgatgaa gacattgtaa gcagagtggc tgaggagatg acatttttcc ccaaagagga 120
gagagttttc tcagataaag gctgcaaaac ggtgttcacc aagtttagatt attactacga 180
tgattgacag tcattgattgg cagcc                                     205

```

```

<210> 28
<211> 19
<212> DNA
<213> Synthetic

```

```

<400> 28
cctggaatac aaacaccta                                     19

```

```

<210> 29

```

<211> 20
 <212> DNA
 <213> Synthetic

<400> 29
 ggctgccaat catgactgtc 20

<210> 30
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 30
 gcaaaacagg gctttgtacc g 21

<210> 31
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 31
 agtagagacg cgggtagatg 20

<210> 32
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 32
 gcgtctctac tgcctcttcg 20

<210> 33
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 33
 atgccctggt cctagttcag 20

<210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 34

ggttttcgcaa ggtgcttgga 20

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 35
 gggattccaa acttccatcc 20

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 36
 tccatgggggt tggtaggaac 20

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 37
 ggtgacagag taaaactatc tg 22

<210> 38
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 38
 gacccccagt agacgtttgt 20

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide

<400> 39
 gtaaaaaatc atgagccctg c 21

<210> 40
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 40

ccagagttag tgagcaggtc 20

<210> 41

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 41

gaagcgtaa ggacctccac 20

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 42

atctatctct gccaatctcc ac 22

<210> 43

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 43

gtcctggtaa acaaagtgct g 21

<210> 44

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide

<400> 44

tggggttact ctatgttggt c 21

<210> 45

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide


```

<400> 45
ctagcacagt atgccctaag                                     20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 46
tgaggaatgt gctgagggtc                                     20

<210> 47
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide

<400> 47
gctgtctcct accccatctg                                     20

<210> 48
<211> 283
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(283)
<223> n = A,T,C or G

<400> 48
gtaggctggg gcgggggctg gaggctgggg ctggggctgg ggctggggcga tggcactagg 60
gctgaactag gaccagggca tggagaatgg aggatggagg ccgggggatg gcaccagggc 120
cgggctagga ctagggctgg agcggggcct gggggctggg gctgggcat ggcactaggg 180
cgggttgggg ctggggctgg ggctggggga tggagcgggg ccgggggctg ggggtggggc 240
tggggggatcg actagggctg gnttaggacc aggcgggttg cat                      283

<210> 49
<211> 375
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(375)
<223> n = A,T,C or G

<400> 49
ggatggtgga tggaggctgg gggatggcag tagggccggg ctaggactgg ggctggagcg 60
gagtttgggg ctggggctca ggagcggggg ctggggctgg ggctggggct gggggatggc 120
actagggcag gccggggtag gggtcacatc ccaggagggc cgggctgggc agagctgagt 180

```

```

ccgcgggggc cggaccccg aagccaagcn gccggcctgc aggatgaggg ctggctcctc 240
ggccatgacc acagacgtgc cagacttaag tacggagacc tgaggagcca ggctgcagtt 300
ggcctacttt ncnctaagct gggggtggac cagtggtaac ctctccgaa gtgggttctg 360
ctctttctag cctag 375

```

```

<210> 50
<211> 439
<212> DNA
<213> Unknown

```

```
<220>
```

```
<223> cDNA clone of DYT1 intron 1
```

```
<221> misc_feature
```

```
<222> (1)...(439)
```

```
<223> n = A,T,C or G
```

```
<400> 50
```

```

ccactgccac tgccaccagt ttgcaccctt aaccctgtg ctgctcctcc caccccaagg 60
cagagccggn gaaaggaaac agtttggtcc ctctgggtcg gctgcggaag agtctcacca 120
tccttctgtc tccgtagcta gaaaggaggg agaaccacac ttcggaggga ggttaccact 180
ggtccacccc cagcttagcg caaagtaggc caacctgcat gcctggnnct cctcaggntc 240
tgcctactta agtctggcag ctctnnntca tggccgaggt agccaggctc atcctgcagg 300
nncngccnn ttgncttncc ggggtntcgn nccccgtac tcagctcgtc cagccggcct 360
ctggatgtga cctaccgctg ctagtgcac ccagccagcc agccagccgt ctagccagcc 420
aactgctcag ccagtctag 439

```

```

<210> 51
<211> 368
<212> DNA
<213> Unknown

```

```
<220>
```

```
<223> cDNA clone of DYT1 intron 1
```

```
<221> misc_feature
```

```
<222> (1)...(368)
```

```
<223> n = A,T,C or G
```

```
<400> 51
```

```

caaagccaat caggagtggg gaagaaacac ggcaaaatgt agccacattt acagcccata 60
aganagccag caaagccgtc tagcctccaa gcaccttgcg aaacctcaag tactgcggtc 120
tggttaagctc ctggcccaga ggggacggcg gtccaggng cctcccttt gctggtcctg 180
cctattctaa agccctggcc cgnctccttc ccgaaaagcc ccttggtgcc actgccactg 240
ccaccanttt gcncccctac cctgtntctg ctctccccc cccaaggcag atgcggnnng 300
ngaaaggaaa cantttggtc cctcctggtc ggctcgnnga agactcctca ccaccccttc 360
tgtcttcc 368

```

```

<210> 52
<211> 400
<212> DNA
<213> Unknown

```

```
<220>
```

```
<223> cDNA clone of DYT1 intron 2
```

```
<400> 52
```

```

gaatatttac gaggggtggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gtttcaaaca tcaccttgta caaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcgggtttt ggggtctctt gttgtgggat gagatttggg agttctatgt 180

```

```

tgaaatgagt gagccccgaa aacggttcat gtctcagttc cccttggaag ggtgtagaag 240
ttaagagttt gagatgcgtg gagcagttaa taccatcaaa gctttgtggg gggttctgaa 300
aatcgggtcca gtgagtatgt agggatcatgg gatttttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat 400

```

```

<210> 53
<211> 418
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 2

```

```

<221> misc_feature
<222> (1)...(418)
<223> n = A,T,C or G

```

```

<400> 53
tttggagtga gacaggactg ggttcaggtc ccagctctgc cacatatagt cttgggcaag 60
tgagtaagc gctctctgtg cctcagttcc ctcactctgta aaatgagaac gatagtgcc 120
actccatggg gttggttaga acaaagaaga ttttgggcat gtaaagtctc tagtgccgag 180
tgcacagtgg tctgtaagtg aagctgcggg tcttagtggt agaaggagct gattgatggc 240
cctggctgag aactttgtgt tcgctttttc cctttttaat tcaggatcag ttacagttgt 300
ggattcgagg caacgtgagt gcctgtgcga ggtccatctt catatttgat gaaatggata 360
agatgcattg aggcctcata gatgcctca ancctttcct cgactattat gacctggt 418

```

```

<210> 54
<211> 198
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 3

```

```

<400> 54
ctcgactatt atgacctggg ggatgggggc tcctaccaga aagccatggt catattttctc 60
aggttaagggt agggcttaga catgatggat gggccccgag cccaagcctc tgagctccag 120
gagaaaaccc tgccttacc cactgggatt gttttgcagc aatgctggag cagaaaggat 180
cacagatgtg tttggatt 198

```

```

<210> 55
<211> 536
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 4

```

```

<221> misc_feature
<222> (1)...(536)
<223> n = A,T,C or G

```

```

<400> 55
gtctgtgtcg gttttcaata acaagaacag gtgagtaggg ccatccaccg ccagtcccat 60
ctggttccta atcctgcacc ctaagtgtta aaagcatcag ggctactgtc agcatcacct 120
gggagctggg tagaaagaaa tggagattct cagtcccctt ccgagtcatt aggggaattc 180
ttgctgatga actccaggta acttttatga acactaatgt ttgacaagtg ctgtttttatt 240
tttatttttc agatagtttt actctgtcac ctaggctgga gtgcagtggc gtaaccttgc 300
ctcactgcaa cctctgcctc ccgggctcaa gcgattcttg tgcctcagcc tcctgagtag 360
ctgggattac aggtgcacac catgcccacg cnaatatatt gtatttttag tagaganggg 420

```

```

gccccgtncatgtttaaccag gctgggtcttg aactnttacc tcaggtgagt ccnccacctc 480
ggcctcccaa agtgctgga ttacaggcgt gagccactgt gtctcagctt attttt 536

```

```

<210> 56
<211> 1302
<212> DNA
<213> Unknown

```

```

<220>
<223> cDNA clone of DYT1 intron 4

```

```

<221> misc_feature
<222> (1)...(1302)
<223> n= A,T,C or G; m= A,or C; r= G,or A; w= A,or T; y= C,or T

```

```

<400> 56
gccactccaa gctaccatct gagattgttt cctgccctag agtggttaaag gcgtgaggtc 60
cgtctgccct cagctgtgtc cccaggccca gggcgtgcct ggcaacanna gcaggcctct 120
gagaaccagc ctccacagtg agttcatgat agnaagacag cccctcgttc ccattcagtg 180
gttggttctg ttcttttcct ggcmataagc tccactctgy mrtcagccam acatttattg 240
agtaccagtt gttggcaaag cactgttggt catgaaaagc attaaccag tgaatgagga 300
ggagcttggg ttgggacgga gccmcaraaw tacatggcag accagaagga aatcagctca 360
agtagaaara cacgcatggg ctctgtggcg acgcagtgtg tgctgtgtca tctggggctg 420
ggaggaagtg tcctggatca ggagttccag gagcccagga ggagtggacg ggtcagtga 480
gagccagccc gcaatcaggg gaagaaaaca cggccaaggc caggccttca cggggagccc 540
agcgtgggct gcacatctgc actctccagg ctagttttgg tgcccacatg ctctgcaggg 600
tctgggcact gtggcagcgg cagcaggctt cctgttgtct agtccagctg ctgaaactcc 660
agggagagtc aaaaagttcc caaatacaga ggcgtggctg gtagtccttc ccgggaattc 720
ttcttgcttc ccgctttctg tggaaactct ccttccccac tctgcctctc tgcttggtcc 780
tgggccccag gacctcttcc ccactcttca tctcttaagt cataccttgg gaggcctccc 840
ccagcccgcc gtgtaaagag ggctgtcaca gcttctgctg tcacagaagc attacaatgt 900
gcaggtgcct gtaacatct gccttcccca ctgatctgga gctccacaag ggagagggca 960
caccagtag gtatgtgtgg gatggatagg aggtgggatg acaccagta gatgtgtatg 1020
ggatggatag gaggggtggat gacaccagtg aggtgtgtat gggatggatg ggagggtggg 1080
tgacccttag tagatgtggg gggggtgggt gggtagcccc cagtaggtgt gtgtggcatg 1140
gataggtgac cccagtaga cgtttgtggg acggtgggga gggtaggtaa gtgaccccca 1200
ggaggcgtct atagggcagg tgggtggatg tggatgaaca gcaccttgtt tcttcttccc 1260
aggtggcttc tggcacagca gcttaattga ccggaacctc at 1302

```

```

<210> 57
<211> 240
<212> DNA
<213> Unknown

```

```

<220>
<223> TORB intron 1-5'

```

```

<221> misc_feature
<222> (1)...(240)
<223> n = A,T,C or G

```

```

<400> 57
ggagcggccg ctcaacgctt cgggtacggc gcgcgcgcga gctgtgggtc ggcgctgcgg 60
ggggcgcggg ggcgcggggg cgcggaggga cggcctcgtg ggcgcctggc acggaccggg 120
cccgtggcat ctagacggcg gtggtcccag ctggggtggg cggggagcgg atggggcgcg 180
cccgaaccg ttgcnggaa cgcagaagcn gtgccttgaa acactctcag atcgtgnggc 240

```

```

<210> 58
<211> 310

```

<212> DNA

<213> Unknown

<220>

<223> TORB intron 1-3'

<221> misc_feature

<222> (1)...(310)

<223> n = A,T,C or G

<400> 58

```

gggaccaaag gacgtccgtc gttcccaccg accctaatacg ttcgcgngtc ngttcgctac 60
ccagtagaga gacttactta cnngtnnatc gaaggaatag tctggggctt cgcaattcct 120
ggaggtgtat tagaactttc accgtagcaa actgacggag ccgggatccc acaccgcctg 180
tgggnncgac acgggacctt ttgacacgaa gaacgaaacn gtcgattctt tcacgacgca 240
acgactacgt aaaaattcca gacaaagaga gaaacaagac cccgacaaga acgtcgagag 300
ttcgacctaa                                     310

```

<210> 59

<211> 401

<212> DNA

<213> Unknown

<220>

<223> TORB intron 2-5'

<221> misc_feature

<222> (1)...(401)

<223> n = A,T,C or G

<400> 59

```

caggaacaac aaaaatccca agaaaccact gaccctttcc ttacacggct gggctggcac 60
aggcaagaat tttgtcagtn aaattgtggc tgaaaaatctt cacccaaaaag gtctgaagag 120
taactttgtc cacctgtttg tatcgactct gcacttccct catgagcaga agataaaaact 180
gtaccaggca agagaacccg ctattatctc gtctgcaggc cagtcggact ggtccgggtg 240
acctgctcac taactctggc ctctgcttct ctttcctttg tgttgctgta gccccgggct 300
ccactgagtt aaggcacact tagtccaggc agttacaaag ctctcctaca acattttctta 360
cttggttcca aaacagtcca gtggggtagg ggatgttatt t                                     401

```

<210> 60

<211> 238

<212> DNA

<213> Unknown

<220>

<223> TORB intron 2-3'

<400> 60

```

ttctgtaact ggtcctggac caaccatgaa agaagaaaca ggatgcgaag ctcaaagggc 60
tgcaccaaga ggcgcgcagg ctccatctgc tcctcatgca ctgaaggacg aggtcagagc 120
tcttagaatg gcaccctcac cccactcgc taggtagcag cttttctaaa accttatctc 180
taaaaagtgg aaattggcag agatagatgc taaaatgcag agaagttttt cctaactc 238

```

<210> 61

<211> 391

<212> DNA

<213> Unknown

<220>

<223> TORB intron 3-5'

<221> misc_feature
 <222> (1)...(391)
 <223> n = A,T,C or G

<400> 61
 gggatcattg acgcaatcaa gccgttttcta gactactacg agcagggttga cggagtgtct 60
 taccgcaaag ccatcttcat ctttctcagg tcagcgggag gcgggtttttt ggggcacaca 120
 agcccttcat tctctcaatg ataaaatgag gtcctgagga ccatcagcac ttgttttacc 180
 aggacgaaag tgccctgcttg gcacaaggca cttacctact gctttacttt tcctttgcca 240
 gtcacacagca tggcacacag tgtgggttgt ggaaatgaac taaagaaata atcactggga 300
 caggcgcggt ggctcacacc tgtcaatccn agcacttttg gnaggcatgg cgggcggatc 360
 acaggagatc gagacatctg ctaacatgnt g 391

<210> 62
 <211> 373
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 3-3'

<221> misc_feature
 <222> (1)...(373)
 <223> n = A,T,C or G

<400> 62
 gtaagacaca gagtcttttt tnttttttag accgagntnc attnttggtg ccnangctgg 60
 agtgcaatgg catgatctcg gctcgctgca acctccacct cccggrttca aacgattctc 120
 ccacctcagc ctcccatgta gctgggatta cagncatgca ccaccattag cctggctaata 180
 ttttgtgttt ttagtagaga tgggggttact ctatgttggt caggctggcc ttgaactccc 240
 gacctcaggt gatctacctg cctcggcctc ccaaagtgtt gggattacag ccatgagcna 300
 ccacnscnan cagacncaga agtccttaata tgtgatttta atctttattt ctctggcaaa 360
 ctcagcaatg cag 373

<210> 63
 <211> 310
 <212> DNA
 <213> Unknown

<220>
 <223> TORB intron 4'

<221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 63
 gtgagtcac cagggtaaag gagcccccta actgtccagc agtgagccgt ctgctctttc 60
 attgagtgtt tgcacaaagc cacaggatcc cactggattt cctcactttg ctaaagtcag 120
 gaattttctt agggcatact gtgctagaaa ccagtgagtg agtggtccagc tgagtcctcg 180
 atgggcttgt tgcacactga caagagacnc tctcaagggg tacggacatg aggaatgtgc 240
 tgagggtcgg gactggagct tggccagggt gcggtggtgg caggaaaccc agctgtgtct 300
 tgttctgcag 310

<210> 64
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide

<400> 64

gaattcctta ag

12

<210> 65

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 5 is a variable residue
Xaa at position 8 is a threonine or a serine
residue

<221> VARIANT

<222> (1)...(8)

<223> Xaa = Any Amino Acid

<400> 65

Gly Xaa Thr Gly Xaa Gly Lys Xaa
1 5

<210> 66

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<223> Xaa at position 2, 3, 4, 8 is a hydrophobic residue
Xaa at position 11 is a variable residue

<221> VARIANT

<222> (1)...(12)

<223> Xaa = Any Amino Acid

<400> 66

Ser Xaa Xaa Xaa Phe Asp Glu Xaa Glu Lys Xaa His
1 5 10

<210> 67

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 67

gtaggctggg

10

<210> 68

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 68

gcaaggatgg

10

<210> 69

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 69

gtaaggtcag

10

<210> 70

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 70

gtgagtaggg

10

<210> 71

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 71

tctttccag

10

<210> 72

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 72

tttaattcag

10

<210> 73

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 73

tgttttgcag

10

<210> 74

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 74

ttcttcccag

10

<210> 75

<211> 11

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 75

cactgcagaa g

11

<210> 76

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of DYT1

<400> 76

caatgctgga

10

<210> 77

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 77

tggcttctgg

10

<210> 78

<211> 10

<212> DNA

<213> Unknown

<220>

<223> Exon/intron of TORB

<400> 78	
gcaagagaac	10
<210> 79	
<211> 10	
<212> DNA	
<213> Unknown	
<220>	
<223> Exon/intron of TORB	
<400> 79	
gtcagcggga	10
<210> 80	
<211> 10	
<212> DNA	
<213> Unknown	
<220>	
<223> Exon/intron of TORB	
<400> 80	
gtgagtccac	10
<210> 81	
<211> 10	
<212> DNA	
<213> Unknown	
<220>	
<223> Exon/intron of TORB	
<400> 81	
gttcttgcag	10
<210> 82	
<211> 10	
<212> DNA	
<213> Unknown	
<220>	
<223> Exon/intron of TORB	
<400> 82	
gttgggtccag	10
<210> 83	
<211> 10	
<212> DNA	
<213> Unknown	
<220>	
<223> Exon/intron of TORB	
<400> 83	
gcaaactcag	10
<210> 84	
<211> 9	

<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 84
tggtctgag 9

<210> 85
<211> 11
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 85
ctctcaagct g 11

<210> 86
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 86
caatgcaggc 10

<210> 87
<211> 10
<212> DNA
<213> Unknown

<220>
<223> Exon/intron of TORB

<400> 87
tggcctgtgg 10

<210> 88
<211> 378
<212> DNA
<213> Unknown

<220>
<223> cDNA clone of DYT1 intron 1

<221> misc_feature
<222> (1)...(378)
<223> n = A,T,C or G

<400> 88
ctgggaaaga caaagccaat caggagtggg gaagaaacac ggcaaaatgt agccacattt 60
acagcccata aganagccag caaagccgtc tagcctccaa gcaccttgcg aaacctcaag 120
tactgcgggc tggtaaagtc ctggcccaga ggggacggcg gtccagggng ccctcccttt 180
gctggctcgt cctattctaa agccctggcc cgnctcctc ccgaaaagcc ccttggtgcc 240

```

actgccactg ccaccanttt gcncccctac ccctgtntctg ctccctcccac cccaaggcag 300
atgcggnnng ngaaaggaaa cantttgggtc cctcctgggtc ggctcgngga agactcctca 360
ccatccttcc tgtcttcc                                     378

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<210> 89
 <211> 402
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 2

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<400> 89
gaatatttac gaggggtgggtc tgaacagtga ctatgtccac ctgtttgtgg ccacattgct 60
ctttccacat gttcaaaca tcaccttgta caaggcaagg atggaagttt ggaatccctt 120
cctggatgtc atcgggtttg ggggtctctt gttgtgggat gagatttggg agttctatgt 180
tgaaatgagt gagcccggaa aacggttcat gtctcagttc cccttggaag ggtgtagaag 240
ttaagagttt gagatgcgtg gagcagttaa taccatcaaa gctttgtggg gggttctgaa 300
aatcgggtcca gtgagtatgt agggtcattg gatttttagag gtggacatga tcaaattccat 360
cttagagatc aacacatctc actcattttt attttcttat tt                                     402

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<210> 90
 <211> 200
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA clone of DYT1 intron 3

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<400> 90
ctcgactatt atgacctggt ggatgggggtc tcctaccaga aagccatggt catattttctc 60
aggtaagggtc agggctagga catgatggat gggccccgag cccaagcctc tgagctccag 120
gagaaaaccc tgtccttacc cactgggatt gttttgcagc aatgctggag cagaaaggat 180
cacagatgtg gctttggatt                                     200

```